

WEST Search History

DATE: Thursday, June 05, 2003

<u>Set Name</u> side by side	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u> result set
<i>DB=USPT,PGPB,JPAB,EPAB,DWPI,TDBD; PLUR=YES; OP=OR</i>			
L6	L5 and adjacent adj5 subsite	3	L6
L5	L4 and heli\$6	70	L5
L4	L3 and random	85	L4
L3	L2 and zinc adj5 polypeptide	121	L3
L2	libr\$6	98851	L2
<i>DB=USPT; PLUR=YES; OP=OR</i>			
L1	6007988.pn.	1	L1

END OF SEARCH HISTORY

and homopurine-homopyrimidine mirror repeats in various prokaryotes, eukaryotes, and an archae-bacterium. Comparison of obsd. frequencies with expectations revealed that in bacterial genomes and organelles the frequency of different repeats is either random or enriched for inverted and/or direct tandem repeats. By contrast, in all eukaryotic genomes studied, the authors obsd. an over-representation of all repeats, esp. homopurine-homopyrimidine mirror repeats. Anal. of the genomic distribution of all abundant repeats showed that they are virtually excluded from coding sequences. Unexpectedly, the frequencies of abundant repeats normalized for their expectations were almost perfect exponential functions of their size, and for a given repeat this function was indistinguishable between different genomes.

L8 ANSWER 2 OF 2 CA COPYRIGHT 2002 ACS
TI The sequence of a large L1Md element reveals a tandemly repeated 5' end and several features found in retrotransposons
AU Loeb, Daniel D.; Padgett, Richard W.; Hardies, Stephen C.; Shehee, W. Ron; Comer, Mary B.; Edgell, Marshall H.; Hutchison, Clyde A., III
SO Mol. Cell. Biol. (1986), 6(1), 168-82
CODEN: MCEBD4; ISSN: 0270-7306
PY 1986
AB The complete nucleotide sequence of a 6851-base-pair (bp) member of the L1Md repetitive family from a selected random isolate of the BALB/c mouse genome is reported. Five kilobases of the element contain 2 overlapping reading frames of 1137 and 3900 bp. The entire 3900-bp frame and the 3' 600 bp of the 1137-bp frame, when compared with a composite primate L1 sequence, show a ratio of replacement to silent site differences characteristic of protein-coding sequences. This more closely defines the protein-coding capacity of this repetitive family, which was previously shown to possess a large open reading frame of underdetd. extent. The relative organization of the 1137- and 3900-bp reading frames, which overlap by 14 bp, bears resemblance to protein-coding, mobile genetic elements. Homol. can be found between the amino acid sequence of the 3900-bp frame and selected domains of several reverse transcriptases. The 5' ends of the 2 L1Md elements described in this report have multiple copies, 4 2/3 copies and 1 2/3 copy of a 208-bp direct tandem repeat. The sequence of this 208-bp element differs from the sequence of a previously defined 5' end for an L1Md element, indicating that there are .gt;eq.2 different 5' end motifs for L1Md.

=> d his

(FILE 'HOME' ENTERED AT 15:34:16 ON 25 OCT 2002)

FILE 'CA' ENTERED AT 15:34:24 ON 25 OCT 2002

L1 10 S ZINC FINGER POLYPEPTIDE
L2 3 S LIBRA?(5W)ZINC(4W)FINGER(4W) (PEPTIDE OR POLYPEPTIDE OR ZIP268
L3 9 S L1 NOT L2
L4 0 S OVERLAP?(5W)RANDOM(5W) (PEPTIDE OR POLYPEPTIDE)
L5 0 S OVERLAP(5W)RANDOM(4W) PEPTIDE
L6 31651 S TANDEM
L7 131 S L6 AND OVERLAP
L8 2 S L7 AND RANDOM